

APR 29 2002

SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: HOGREFE, Holly
- (ii) TITLE OF INVENTION: Polymerase Enhancing Factor (PEF) Extracts, PEF Protein Complexes, Isolated PEF Proteins, and Methods for Purifying and Identifying Same
- (iii) NUMBER OF SEQUENCES: 61
- (iv) CORRESPONDENCE ADDRESS:
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  - (B) STREET: 1300 I Street, N.W.
  - (C) CITY: Washington
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  - (F) ZIP: 20005-3315
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER IBM PC Compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/631,613
  - (B) FILING DATE: 04-AUG-2000
  - (C) CLASSIFICATION:
- (vii) PRIORITY APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/822,774
  - (B) FILING DATE: 21-MAR-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: BARKER, M. Paul
  - (B) REGISTRATION NUMBER: 32,013
  - (C) REFERENCE/DOCKET NUMBER: 4121.0116-07
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa	Xaa	Leu	His	His	Val	Lys	Leu	Ile	Tyr	Ala	Thr	Xaa	Xaa	Xaa
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa	Xaa	Xaa	Pro	Asp	Trp	Xaa	Xaa	Arg	Xaa	Glu	Xaa	Leu	Xaa	Xaa
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa	Leu	Leu	His	His	Val	Lys	Leu	Ile	Tyr	Ala	Thr	Lys	Xaa	Arg	Xaa
1				5					10						15

Leu	Val	Gly	Lys	Xaa	Ile	Val	Leu	Ala	Ile	Pro	Gly	Xaa	Xaa	Ala	Xaa
			20						25					30	

Xaa Xaa Xaa

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (v) FRAGMENT-TYPE: N-terminal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa	Xaa	Xaa	Pro	Asp	Trp	Xaa	Xaa	Arg	Xaa	Glu	Xaa	Leu	Xaa	Glu	Xaa
1				5				10						15	

Xaa Xaa

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (v) FRAGMENT-TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa	Tyr	Asp	Ala	Val	Ile	Met	Ala	Ala	Ala	Val	Val	Asp	Phe	Arg	Pro
1				5				10						15	

Lys

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu  
1                      5                      10                      15  
  
Asn Gln Val Val Leu Ile Gly Arg  
                    20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Xaa Lys Leu Arg  
1                      5                      10                      15  
  
Lys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 18 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Xaa  
1 5 10 15

Arg Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Lys Phe Arg Lys Glu Glu Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Ala	Ile	Leu	Leu	Pro	Asp	Trp	Lys	Ile	Arg	Lys	Glu	Ile	Leu	Ile
1			5					10					15		

Glu

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa	Met	His	His	Val	Ile	Lys	Leu	Xaa	Tyr	Ala	Thr	Xaa	Ser	Arg	Lys
1				5				10					15		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Leu Tyr Leu Val Arg Pro Asp Trp Lys Arg Arg Lys Glu Ile Leu  
1                      5                      10                      15  
  
Ile Glu

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAYCAYGAHA ARYTHATTTA CGC

23

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCATDATNA CDGCRTC GTA TTT

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAYCAYGAHA ARYTHATATA CGC

23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ARDACDACYT GRTTTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1209 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCTTCACC ACGTCAAGCT AATCTACGCC ACAAAAAGTC GAAAGCTAGT TGGAAAAAAG	60
ATAGTCNNNN NNNNNCCAGG GAGTATTGCG GCTTTGGATG TGAAAGCTTG TGAGGGACTA	120
ATTAGGCATG GGGCCGAAGT TCATGCAGTG ATGAGTGAGG CAGCCACCAA GATAATTCAT	180
CCTTATGCAT GGAATTTGCC CACGGGAAAT CCAGTCATAA CTGAGATCAC TGGATTTTATC	240



GAGCATGTTG AGTTAGCAGG GGAACATGAG AATAAAGCAG ATTTAATTTT GGTTTGTCTT	300
GCCACTGCCA ACACAATTAG TAAGATTGCA TGTGGAATAG ATGATACTCC AGTAACTACA	360
GTCGTGACCA CAGCATTTCC CCACATTCCA ATTATGATAG CCCCAGCAAT GCATGAGACA	420
ATGTACAGGC ATCCCATAGT AAGGGAGAAC ATTGAAAGGT TAAAGAAGCT TGGCGTTGAG	480
TTTATAGGAC CAAGAATTGA GGAGGGAAAG GCAAAAGTTG CAAGCATTGA TGAAATAGTT	540
TACAGAGTTA TTAAAAAGCT CCACAAAAAA ACATTGGAAG GGAAGAGAGT CCTAGTAACG	600
GCGGGAGCAA CAAGAGAGTA CATAGATCCA ATAAGATTCA TAACAAATGC CAGCAGTGGA	660
AAAATGGGAG TAGCGTTGGC TGAAGAAGCA GATTTTAGAG GAGCTGTTAC CCTCATAAGA	720
ACAAAGGGAA GTGTAAAGGC TTTTAGAATC AGAAAAATCA AATTGAAGGT TGAGACAGTG	780
GAAGAAATGC TTTCAGCGAT TGAAAATGAG TTGAGGAGTA AAAAGTATGA CGTAGTTATT	840
ATGGCAGCTG CTGTAAGCGA TTTTAGGCCA AAAATTAAAG CAGAGGGAAA AATTAAAAGC	900
GGAAGATCAA TAACGATAGA GCTCGTTCCN NNNAATCCCA AAATCATTGA TAGAATAAAG	960
GAAATTCAAC CAAATGTCTT TCTTGTTGGA TTTAAAGCAG AAACCTCAAA AGAAAAGCTT	1020
ATAGAAGAAG GTAAAAGGCA GATTGAGAGG GCCAAGGCTG ACTTAGTCGT TGGTAACACA	1080
TTGGAAGCCT TTGGAAGCGA GGAAAACCAA GTAGTATTAA TTGGCAGAGA TTTCACAAAA	1140
GAACCTCCAA AAATGAAAAA GAGAGAGTTA GCAGAGAGAA TTTGGGATGA GATAGAGAAA	1200
TTNCTGTCC	1209

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 403 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Leu	His	His	Val	Lys	Leu	Ile	Tyr	Ala	Thr	Lys	Ser	Arg	Lys	Leu
1				5				10						15	
Val	Gly	Lys	Lys	Ile	Val	Xaa	Xaa	Xaa	Pro	Gly	Ser	Ile	Ala	Ala	Leu
			20					25						30	
Asp	Val	Lys	Ala	Cys	Glu	Gly	Leu	Ile	Arg	His	Gly	Ala	Glu	Val	His
			35				40					45			

Ala 50	Val	Met	Ser	Glu	Ala 55	Ala	Thr	Lys	Ile	Ile 60	His	Pro	Tyr	Ala	Trp
Asn 65	Leu	Pro	Thr	Gly	Asn 70	Pro	Val	Ile	Thr	Glu 75	Ile	Thr	Gly	Phe	Ile 80
Glu	His	Val	Glu	Leu 85	Ala	Gly	Glu	His	Glu 90	Asn	Lys	Ala	Asp	Leu 95	Ile
Leu	Val	Cys	Pro 100	Ala	Thr	Ala	Asn	Thr 105	Ile	Ser	Lys	Ile	Ala 110	Cys	Gly
Ile	Asp	Asp 115	Thr	Pro	Val	Thr	Thr 120	Val	Val	Thr	Thr	Ala 125	Phe	Pro	His
Ile 130	Pro	Ile	Met	Ile	Ala	Pro 135	Ala	Met	His	Glu	Thr 140	Met	Tyr	Arg	His
Pro 145	Ile	Val	Arg	Glu	Asn 150	Ile	Glu	Arg	Leu	Lys 155	Lys	Leu	Gly	Val	Glu 160
Phe	Ile	Gly	Pro	Arg 165	Ile	Glu	Glu	Gly	Arg 170	Ala	Lys	Val	Ala	Ser 175	Ile
Asp	Glu	Ile	Val 180	Tyr	Arg	Val	Ile	Lys 185	Lys	Leu	His	Lys	Lys 190	Thr	Leu
Glu	Gly	Lys 195	Arg	Val	Leu	Val	Thr 200	Ala	Gly	Ala	Thr	Arg 205	Glu	Tyr	Ile
Asp	Pro 210	Ile	Arg	Phe	Ile	Thr 215	Asn	Ala	Ser	Ser	Gly 220	Lys	Met	Gly	Val
Ala 225	Leu	Ala	Glu	Glu	Ala 230	Asp	Phe	Arg	Gly	Ala 235	Val	Thr	Leu	Ile	Arg 240
Thr	Lys	Gly	Ser	Val 245	Lys	Ala	Phe	Arg	Ile 250	Arg	Lys	Ile	Lys	Leu 255	Lys
Val	Glu	Thr	Val 260	Glu	Glu	Met	Leu	Ser 265	Ala	Ile	Glu	Asn	Glu 270	Leu	Arg
Ser	Lys	Lys 275	Tyr	Asp	Val	Val	Ile 280	Met	Ala	Ala	Ala	Val 285	Ser	Asp	Phe
Arg	Pro 290	Lys	Ile	Lys	Ala	Glu 295	Gly	Lys	Ile	Lys	Ser 300	Gly	Arg	Ser	Ile
Thr 305	Ile	Glu	Leu	Val	Pro 310	Xaa	Asn	Pro	Lys	Ile 315	Ile	Asp	Arg	Ile	Lys 320
Glu	Ile	Gln	Pro	Asn 325	Val	Phe	Leu	Val	Gly 330	Phe	Lys	Ala	Glu	Thr 335	Ser
Lys	Glu	Lys	Leu 340	Ile	Glu	Glu	Gly	Lys 345	Arg	Gln	Ile	Glu	Arg	Ala	Lys 350

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu  
355 360 365

Asn Gln Val Val Leu Ile Gly Arg Asp Phe Thr Lys Glu Leu Pro Lys  
370 375 380

Met Lys Lys Arg Glu Leu Ala Glu Arg Ile Trp Asp Glu Ile Glu Lys  
385 390 395 400

Xaa Leu Ser

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATAGCGAAT TCGCAAAC TTTGCGGTA TGG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTACGGAAT TCCACGAAA ATGCCGCTCA TCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCGTTTCCG TTCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATCTCACG CGCCAGTTTC

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCTTGCTC AACTTTATC

19

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATAGAGATA GTTCTGGAG ACG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGATATCG ACATTTCTGC ACC

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAGTTAAATG CCTACACTGT ATCT

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGACTCAG AAGCTGCTAT CGAA

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCACGTGC CCTGTAGGAT TTGT

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCAGAYTGGA ARWKNAGGAA AGA

23

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCAGAYTGGA ARWKNAGAAA AGA

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCAGAYTGGA ARWKNAGGAA GGA

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCAGAYTGGA ARWKNAGAAA GGA

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGAGTGGGC AGAGAGGCTN TTGTTAAGGG GAAATTAATC GACGTGGAAA AGGAAGGAAA

60

AGTCGNTATT CCTCCAAGGG AATA

84

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Trp Ala Glu Arg Leu Leu Arg Gly Asn Xaa Ser Lys Trp Lys  
1 5 10 15

Arg Lys Glu Lys Ser Xaa Phe Leu Gln Gly Asn  
20 25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Val Gly Arg Glu Ala Xaa Val Lys Gly Lys Leu Ile Glu Val Glu

1 5 10 15

Lys Glu Gly Lys Val Xaa Ile Pro Pro Arg Glu  
20 25

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gln Ser Gly Gln Arg Gly Xaa Cys Xaa Gly Glu Ile Asn Arg Ser Gly  
1 5 10 15

Lys Gly Arg Lys Ser Arg Tyr Ser Ser Lys Gly Leu  
20 25

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCCCACTC TGAGGTCATA ACCTGCTGGT TGGAGCCATT CTTGAGAAAA TGGCTCTATA 60  
AGTATTTCTT TTCTGATTTT CCAGTCTGGA AGTAGCATTT TACCACCGAA ACCTTTATTT 120  
TTAATTTAA 129

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Xaa	Ile	Lys	Asn	Lys	Gly	Phe	Gly	Gly	Lys	Met	Leu	Leu	Pro	Asp	Trp
1				5					10					15	
Lys	Ile	Arg	Lys	Glu	Ile	Leu	Ile	Glu	Pro	Phe	Ser	Glu	Glu	Trp	Leu
			20					25					30		
Gln	Pro	Ala	Gly	Tyr	Asp	Leu	Arg	Val	Gly						
			35					40							

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 740 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCCTCCAAGG GAATACGCCT TAATCCTAAC CCTCGAGAGG ATAAAGTTGC CCGACGATGT	60
TATGGGGGAT ATGAAGATAA GGAGCAGTTT AGCAAGAGAA GGGGTTATTG GTTCTTTTGC	120
TTGGGTTGAC CCAGGATGGG ATGGAACTT AACACTAATG CTCTACAATG CCTCAAATGA	180
ACCTGTCGAA TTAAGATATG GAGAGAGATT TGTGCAGATC GCATTTATAA GGCTAGAGGG	240
TCCGGCAAGA AACCTTACA GAGGAACTA TCAGGGGAGC ACAAGGTTAG CGTTTTCAAA	300
GAGAAAGAAA CTCTAGCGTC TTTTCAATAG CATCCTCAAT ATCTCGTGTG AAGTAATCAA	360
TGTAAATACT TGCTGGGTGG GTTTTTAGGG ATTCAAATC GTAAGATGGG CCTGTATAGC	420

AGAAACTAT TTTTGCCTCT TCTTCATTTA TCTTTCTGTG AATAAAAAAT CCAACATCCA	480
CACTAGTTCC AAAAGATATT GTTTGCGTGA TTACCAACAA GATCTTGGCA TTATTTTGA	540
TCTTATACTC TATTCTCCTT TCTCCCTCCA ATTTGCCCAA AATAAACCTG GG TAGTATAC	600
ATTCACTCCT CTCTTTTAAA TTCCTATAAA TTCGTACATA GTTTAGAAAA ATGTCAAATT	660
CTTTNTTCCC TGTAAATTA ACCNCNAAAT CTTTATNANN AANCTTTTTA TAATTCCCAA	720
AACCCCTAAT TTTCCCTTN	740

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 246 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT-TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Leu	Gln	Gly	Asn	Thr	Pro	Xaa	Ser	Xaa	Pro	Ser	Arg	Gly	Xaa	Ser	Cys
1				5					10					15	
Pro	Thr	Met	Leu	Trp	Gly	Ile	Xaa	Arg	Xaa	Gly	Ala	Val	Xaa	Gln	Glu
			20					25					30		
Lys	Gly	Leu	Leu	Val	Leu	Leu	Leu	Gly	Leu	Thr	Gln	Asp	Gly	Met	Glu
		35					40					45			
Thr	Xaa	His	Xaa	Cys	Ser	Thr	Met	Pro	Gln	Met	Asn	Leu	Ser	Asn	Xaa
	50					55					60				
Asp	Met	Glu	Arg	Asp	Leu	Cys	Arg	Ser	His	Leu	Xaa	Gly	Xaa	Arg	Val
65					70					75				80	
Arg	Gln	Glu	Thr	Leu	Thr	Glu	Glu	Thr	Ile	Arg	Gly	Ala	Gln	Gly	Xaa
				85					90					95	
Arg	Phe	Gln	Arg	Glu	Arg	Asn	Ser	Ser	Val	Phe	Ser	Ile	Ala	Ser	Ser
			100					105					110		
Ile	Ser	Arg	Val	Lys	Xaa	Ser	Met	Xaa	Ile	Leu	Ala	Gly	Trp	Val	Phe
		115					120					125			
Arg	Asp	Ser	Asn	Ser	Xaa	Asp	Gly	Pro	Val	Xaa	Gln	Lys	Thr	Ile	Phe

130		135		140
Ala Ser Ser Ser Phe Ile Phe Leu Xaa Ile Lys Asn Pro Thr Ser Thr				
145		150	155	160
Leu Val Pro Lys Asp Ile Val Cys Val Ile Thr Asn Lys Ile Leu Ala				
	165		170	175
Leu Phe Leu Ile Leu Tyr Ser Ile Leu Leu Ser Pro Ser Asn Leu Pro				
	180	185		190
Lys Ile Asn Leu Gly Ser Ile His Ser Leu Leu Ser Phe Lys Phe Leu				
	195	200		205
Xaa Ile Arg Thr Xaa Phe Arg Lys Met Ser Asn Ser Xaa Phe Pro Val				
	210	215	220	
Lys Leu Thr Xaa Lys Ser Leu Xaa Xaa Xaa Phe Leu Xaa Phe Pro Lys				
225		230	235	240
Pro Leu Ile Phe Pro Xaa				
	245			

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 246 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu Arg Ile Lys Leu				
1	5	10	15	
Pro Asn Asn Val Met Gly Asp Met Lys Ile Arg Ser Ser Leu Ala Arg				
	20	25	30	
Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro Gly Trp Asp Gly				
	35	40	45	
Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu Pro Val Glu Leu				
	50	55	60	
Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile Arg Leu Glu Gly				
65	70	75	80	
Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly Ser Thr Arg Leu				
	85	90	95	
Ala Phe Ser Lys Arg Lys Lys Leu Xaa Arg Leu Phe Asn Ser Ile Leu				

100	105	110
Asn Ile Ser Cys Glu Val Ile	Asn Val Asn Thr Cys Trp Val Gly Phe	
115	120	125
Xaa Gly Phe Lys Leu Val Arg Trp Ala Cys Ile Ala Glu Asn Tyr Phe		
130	135	140
Cys Leu Phe Phe Ile Tyr Leu Ser Val Asn Lys Lys Ser Asn Ile His		
145	150	155
Thr Ser Ser Lys Arg Tyr Cys Leu Arg Asp Tyr Gln Gln Asp Leu Gly		
165	170	175
Ile Ile Phe Asp Leu Ile Leu Tyr Ser Pro Phe Ser Leu Gln Phe Ala		
180	185	190
Gln Asn Lys Pro Gly Xaa Tyr Thr Phe Thr Pro Leu Phe Xaa Ile Pro		
195	200	205
Ile Asn Ser Tyr Ile Val Xaa Lys Asn Val Lys Phe Phe Xaa Pro Cys		
210	215	220
Xaa Ile Asn Xaa Xaa Ile Phe Xaa Xaa Xaa Leu Phe Ile Ile Pro Lys		
225	230	235
Thr Pro Asn Phe Pro Leu		
245		

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 246 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Ser Lys Gly Ile Arg Leu Asn Pro Asn Pro Arg Glu Asp Lys Val		
1	5	10
Ala Arg Arg Cys Tyr Gly Gly Tyr Glu Asp Lys Glu Gln Phe Ser Lys		
20	25	30
Arg Arg Gly Tyr Trp Phe Phe Cys Leu Gly Xaa Pro Arg Met Gly Trp		
35	40	45
Lys Leu Asn Thr Asn Ala Leu Gln Cys Leu Lys Xaa Thr Cys Arg Ile		
50	55	60
Lys Ile Trp Arg Glu Ile Cys Ala Asp Arg Ile Tyr Lys Ala Arg Gly		



Val Gly Lys Lys Ile Val Xaa Xaa Xaa Pro Gly Ser Ile Ala Ala  
20 25 30

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Tyr Asp Val Val Ile Met Ala Ala Ala Val Ser Asp Phe Arg Phe  
1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu  
1 5 10 15

Asn Gln Val Val Leu Ile Gly Arg  
20

(2) INFORMATION FOR SEQ ID NO:49:



(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Methanococcus Jannaschii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Ile	Ser	Glu	Ile	Met	His	Pro	Thr	Lys	Leu	Leu	Lys	Gly	Thr	Lys	1	5	10	15
Ser	Lys	Leu	Leu	Glu	Asn	Lys	Lys	Ile	Leu	Val	Ala	Val	Thr	Ser	Ser	20	25	30	
Ile	Ala	Ala	Ile	Glu	Thr	Pro	Lys	Leu	Met	Arg	Glu	Leu	Ile	Arg	His	35	40	45	
Gly	Ala	Glu	Val	Tyr	Cys	Ile	Ile	Thr	Glu	Glu	Thr	Lys	Lys	Ile	Ile	50	55	60	
Gly	Lys	Glu	Ala	Leu	Lys	Phe	Gly	Cys	Gly	Asn	Glu	Val	Tyr	Glu	Glu	65	70	75	80
Ile	Thr	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Ile	Glu	His	Ile	Leu	Leu	Tyr	85	90	95	
Xaa	Xaa	Xaa	Xaa	Asn	Glu	Cys	Asp	Cys	Leu	Leu	Ile	Tyr	Pro	Ala	Thr	100	105	110	
Ala	Asn	Ile	Ile	Ser	Lys	Ile	Asn	Leu	Gly	Ile	Ala	Asp	Asn	Ile	Val	115	120	125	
Asn	Thr	Thr	Ala	Leu	Met	Phe	Phe	Gly	Asn	Lys	Pro	Ile	Phe	Ile	Val	130	135	140	
Pro	Ala	Met	His	Glu	Asn	Met	Phe	Asn	Xaa	Xaa	Ala	Ile	Lys	Arg	His	145	150	155	160
Ile	Asp	Lys	Leu	Lys	Glu	Lys	Asp	Lys	Ile	Tyr	Ile	Ile	Ser	Pro	Lys	165	170	175	
Phe	Glu	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Lys	Ala	Lys	Val	Ala	Asn	180	185	190	
Ile	Glu	Asp	Val	Val	Lys	Ala	Val	Ile	Glu	Lys	Ile	Gly	Asn	Asn	Leu	195	200	205	
Lys	Lys	Glu	Gly	Asn	Arg	Val	Leu	Ile	Leu	Asn	Gly	Gly	Thr	Val	Glu	210	215	220	
Phe	Ile	Asp	Lys	Val	Arg	Val	Ile	Ser	Asn	Leu	Ser	Ser	Gly	Lys	Met	225	230	235	240
Gly	Val	Ala	Leu	Ala	Glu	Ala	Phe	Cys	Lys	Glu	Gly	Phe	Tyr	Val	Glu	245	250	255	
Val	Ile	Thr	Ala	Met	Gly	Leu	Glu	Pro	Pro	Tyr	Tyr	Ile	Lys	Asn	His	260	265	270	
Lys	Val	Leu	Thr	Ala	Lys	Glu	Met	Leu	Asn	Lys	Ala	Ile	Glu	Xaa	Xaa	275	280	285	
Leu	Xaa	Ala	Lys	Asp	Phe	Asp	Ile	Ile	Ile	Ser	Ser	Ala	Ala	Ile	Ser	290	295	300	

Asp Phe Thr Val Glu Ser Xaa Phe Glu Gly Lys Leu Ser Ser Glu Glu  
 305 310 315 320  
 Glu Xaa Xaa Xaa Xaa Leu Ile Leu Lys Leu Lys Arg Xaa Asn Pro Lys  
 325 330 335  
 Val Leu Glu Glu Leu Arg Arg Ile Tyr Lys Asp Xaa Lys Val Ile Ile  
 340 345 350  
 Gly Phe Lys Ala Glu Tyr Asn Leu Asp Glu Lys Glu Leu Ile Asn Arg  
 355 360 365  
 Ala Lys Glu Arg Leu Asn Lys Tyr Asn Leu Asn Met Ile Ile Ala Asn  
 370 375 380  
 Asp Leu Ser Lys Xaa Xaa His Tyr Phe Gly Asp Asp Tyr Ile Glu Val  
 385 390 395 400  
 Tyr Ile Ile Thr Lys Tyr Glu Val Glu Lys Ile Ser Gly Ser Lys Lys  
 405 410 415  
 Xaa Glu Ile Ser Glu Arg Ile Val Glu Lys Val Lys Lys Leu Val Lys  
 420 425 430  
 Ser Xaa Xaa Xaa Xaa  
 435

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ala Arg Gln Gln Lys Tyr Cys Asp Lys Ile Ala Asn Phe Trp  
 1 5 10 15  
 Cys His Pro Thr Gly Lys Ile Ile Met Ser Leu Ala Gly Lys Lys Ile  
 20 25 30  
 Val Leu Gly Val Ser Gly Gly Ile Ala Ala Tyr Lys Thr Pro Glu Leu  
 35 40 45  
 Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr  
 50 55 60

Glu	Ala	Ala	Lys	Ala	Phe	Ile	Thr	Pro	Leu	Ser	Leu	Gln	Ala	Val	Ser	
65					70					75					80	
Gly	Tyr	Pro	Val	Ser	Asp	Ser	Leu	Leu	Asp	Pro	Ala	Ala	Glu	Ala	Ala	
				85					90					95		
Met	Gly	His	Ile	Glu	Leu	Gly	Xaa	Xaa	Xaa	Xaa	Lys	Trp	Ala	Asp	Leu	
			100					105						110		
Val	Ile	Leu	Ala	Pro	Ala	Thr	Ala	Asp	Leu	Ile	Ala	Arg	Val	Ala	Ala	
		115					120					125				
Gly	Met	Ala	Asn	Asp	Leu	Val	Ser	Thr	Ile	Cys	Leu	Ala	Thr	Pro	Xaa	
	130					135						140				
Xaa	Ala	Pro	Val	Ala	Val	Leu	Pro	Ala	Met	Asn	Gln	Gln	Met	Tyr	Arg	
145					150					155					160	
Ala	Ala	Ala	Thr	Gln	His	Asn	Leu	Glu	Val	Leu	Ala	Xaa	Ser	Arg	Gly	
				165					170					175		
Leu	Leu	Ile	Trp	Gly	Pro	Asp	Ser	Gly	Ser	Gln	Ala	Cys	Gly	Asp	Ile	
			180					185					190			
Gly	Pro	Gly	Arg	Xaa	Xaa	Asp	Pro	Leu	Thr	Ile	Val	Asp	Met	Ala	Val	
		195					200					205				
Ala	His	Phe	Ser	Pro	Val	Asn	Asp	Leu	Lys	His	Leu	Asn	Ile	Met	Ile	
	210					215					220					
Thr	Ala	Gly	Pro	Thr	Arg	Glu	Pro	Leu	Asp	Pro	Val	Arg	Tyr	Ile	Ser	
225					230					235					240	
Asn	His	Ser	Ser	Gly	Lys	Met	Gly	Phe	Ala	Ile	Ala	Ala	Ala	Ala	Ala	
				245				250						255		
Arg	Arg	Gly	Ala	Asn	Val	Thr	Leu	Val	Ser	Gly	Pro	Val	Ser	Leu	Pro	
			260					265					270			
Thr	Pro	Pro	Phe	Val	Lys	Arg	Val	Asp	Val	Met	Thr	Ala	Leu	Glu	Met	
		275					280					285				
Glu	Ala	Ala	Val	Asn	Xaa	Xaa	Ala	Ser	Val	Gln	Gln	Gln	Asn	Ile	Phe	
	290					295					300					
Ile	Gly	Cys	Ala	Ala	Val	Ala	Asp	Tyr	Arg	Ala	Ala	Thr	Val	Ala	Pro	
305					310					315					320	
Glu	Lys	Ile	Lys	Lys	Gln	Ala	Thr	Gln	Gly	Asp	Glu	Leu	Thr	Ile	Lys	
				325					330					335		
Met	Val	Lys	Xaa	Asn	Pro	Asp	Ile	Val	Ala	Gly	Val	Ala	Ala	Leu	Lys	
			340					345				350				
Asp	His	Arg	Pro	Tyr	Val	Val	Gly	Phe	Ala	Ala	Glu	Thr	Asn	Asn	Xaa	
	355						360					365				

Xaa Xaa Xaa Val Glu Glu Tyr Ala Arg Gln Lys Arg Ile Arg Lys Asn  
 370 375 380  
 Leu Asp Leu Ile Cys Ala Asn Asp Val Ser Gln Pro Thr Gln Gly Phe  
 385 390 395 400  
 Asn Ser Asp Asn Asn Ala Leu His Leu Phe Trp Gln Asp Gly Asp Lys  
 405 410 415  
 Val Leu Pro Leu Glu Arg Lys Glu Leu Leu Gly Gln Leu Leu Leu Asp  
 420 425 430  
 Glu Ile Val Thr Arg Tyr Asp Glu Lys Asn Arg Arg  
 435 440

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa  
 1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ala Val His Asp Pro Gly Tyr Glu Gly Arg Pro Glu Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Thr Ile Val Asp Ala Gly Phe Glu Gly Gln Leu Thr Ile  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala His Arg Ile Asp Pro Gly Trp Ser Gly Cys Ile Val Leu  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:  
GAGTTAAATG CCTACACTGT ATCT

24

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:  
CAGGACTCAG AAGCTGCTAT CGAA

24

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:  
CTGCACGTGC CCTGTAGGAT TTGT

24